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1

SEQUENCE LISTING

<110> Dr. Völkel, Helge

<120> Method for screening of modulators of calcineurin activity

<130> A34157PCT

<140> PCT/EP99/05220

<141> 1999-07-22

<150> EP98113876

<151> 1998-07-22

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<170> PatentIn Ver. 2.1

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- 12 -

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 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
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 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
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 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
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 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
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 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
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 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
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 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
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 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
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**SUBSTITUTE SHEET (RULE 26)**

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&lt;222&gt; (1330)..(2916)

&lt;223&gt; calcineurin A beta

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Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
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Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
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 115 120 125  
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
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 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
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Ser Ile Ile Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr						
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Gly Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu Ser Glu Ser						
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**SUBSTITUTE SHEET (RULE 26)**

**THE** **NEW** **YORK** **PUBLIC** **LIBRARY**

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Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys				
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ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag				1083
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys				
	145	150	155	
cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag				1131
Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu				
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Tyr Lys Ser Gly Leu Arg Ser Arg Ser Met Ser Gly Arg Arg Phe His				
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Gln Arg Leu Thr Phe Lys Glu Val Phe Glu Asn Gly Lys Pro Lys Val				
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Lys Thr Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys Gly Asp Ile				
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His Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser				
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															1		
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Arg Gly Ser His His His His His His Gly Ser Met Ser Glu Pro Lys																	
										5	10	15					
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Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys Glu Val Phe Asp Asn																	
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Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala His Leu Met Lys Glu																	
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Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile Ile Thr Glu Gly Ala																	
										70	75	80					
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Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp Ile Asp Ala Pro Val																	
										85	90	95					
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Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe Asp Leu Met Lys Leu																	
										100	105	110					
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Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg Tyr Leu Phe Leu Gly																	
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Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn Asn Leu Leu Ser Ile	
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 <212> PRT  
 <213> Homo sapiens

<400> 18

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Val	Pro	Phe	Pro	Pro	Ser	His	Arg	Leu	Thr	Ala	Lys	Glu	Val	Phe	Asp	35	40	45	
Asn	Asp	Gly	Lys	Pro	Arg	Val	Asp	Ile	Leu	Lys	Ala	His	Leu	Met	Lys	50	55	60	
Glu	Gly	Arg	Leu	Glu	Glu	Ser	Val	Ala	Leu	Arg	Ile	Ile	Thr	Glu	Gly	65	70	75	80
Ala	Ser	Ile	Leu	Arg	Gln	Glu	Lys	Asn	Leu	Leu	Asp	Ile	Asp	Ala	Pro	85	90	95	
Val	Thr	Val	Cys	Gly	Asp	Ile	His	Gly	Gln	Phe	Phe	Asp	Leu	Met	Lys	100	105	110	
Leu	Phe	Glu	Val	Gly	Gly	Ser	Pro	Ala	Asn	Thr	Arg	Tyr	Leu	Phe	Leu	115	120	125	
Gly	Asp	Tyr	Val	Asp	Arg	Gly	Tyr	Phe	Ser	Ile	Glu	Cys	Val	Leu	Tyr	130	135	140	
Leu	Trp	Ala	Leu	Lys	Ile	Leu	Tyr	Pro	Lys	Thr	Leu	Phe	Leu	Leu	Arg	145	150	155	160
Gly	Asn	His	Glu	Cys	Arg	His	Leu	Thr	Glu	Tyr	Phe	Thr	Phe	Lys	Gln	165	170	175	
Glu	Cys	Lys	Ile	Lys	Tyr	Ser	Glu	Arg	Val	Tyr	Asp	Ala	Cys	Met	Asp	180	185	190	
Ala	Phe	Asp	Cys	Leu	Pro	Leu	Ala	Ala	Leu	Met	Asn	Gln	Gln	Phe	Leu	195	200	205	
Cys	Val	His	Gly	Gly	Leu	Ser	Pro	Glu	Ile	Asn	Thr	Leu	Asp	Asp	Ile	210	215	220	
Arg	Lys	Leu	Asp	Arg	Phe	Lys	Glu	Pro	Pro	Ala	Tyr	Gly	Pro	Met	Cys	225	230	235	240

Asp Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly Asn Glu Lys Thr  
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 Gln Glu His Phe Thr His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr  
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 Ser Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn Asn Leu Leu Ser  
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 Ile Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr Arg  
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 Lys Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr Ile Phe Ser Ala  
 305 310 315 320  
 Pro Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala Val Leu Lys Tyr  
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 Glu Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro  
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 Tyr Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp Ser Leu Pro Phe  
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 Ser Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe Asp Gly Ala Thr  
 385 390 395 400  
 Ala Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile Arg Ala Ile Gly  
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 Lys Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu Ser Glu Ser Val  
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 Glu Ala Asp Glu Ala Ile Lys Gly Phe Ser Pro Gln His Lys Ile Thr  
 465 470 475 480  
 Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile Asn Glu Arg Met Pro  
 485 490 495  
 Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn Leu Asn Ser Ile Asn  
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 Lys Ala Leu Thr Ser Glu Thr Asn Gly Thr Asp Ser Asn Gly Ser Asn  
 515 520 525  
 Ser Ser Asn Ile Gln  
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&lt;210&gt; 19

&lt;211&gt; 170

&lt;212&gt; PRT

-45-

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

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 35 40 45

Leu Gln Gln Asn Pro Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
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Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Gly Val Ser  
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Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
 85 90 95

Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
 100 105 110

Phe Gln Val Leu Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
 115 120 125

Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Gly  
 130 135 140

Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Gly Gly Leu  
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Asp Ile His Lys Lys Met Val Val Asp Val  
 165 170

&lt;210&gt; 20

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;222&gt; (115)..(1686)

&lt;223&gt; histidine tagged calcineurin A alpha2

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1687)..(1728)

&lt;223&gt; ribosomal binding site, multiple cloning site 2

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1729)..(2241)

&lt;223&gt; calcineurin B

&lt;400&gt; 20

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 Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly Asn Glu Lys Thr Gln  
 245 250 255

gaa cat ttc act cac aac aca gtc agg ggg tgt tca tac ttc tac agt 933  
 Glu His Phe Thr His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr Ser  
 260 265 270

tac ccg gct gta tgt gaa ttc tta cag cac aat aac ttg tta tct ata 981  
 Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn Asn Leu Leu Ser Ile  
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ctc cga gcc cac gaa gcc caa gat gca ggg tac cgc atg tac agg aaa 1029  
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aat gag agg atg ccg cct cgc aga gat gcc atg ccc tct gac gcc aac 1605

Asn Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn  
 485 490 495

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 515 520

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&lt;211&gt; 523

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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 Cys Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr Leu Asp Asp Ile  
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 225 230 235 240  
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 Gln Glu His Phe Thr His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr  
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Pro Gln His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg  
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Leu Gln Gln Asn Pro Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
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Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Gly Val Ser  
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Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
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Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
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Phe Gln Val Leu Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
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Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Gly  
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Asp Ile His Lys Lys Met Val Val Asp Val  
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&lt;223&gt; histidine tagged calcineurin A betal

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&lt;223&gt; ribosomal binding site, multiple cloning site 2

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&lt;222&gt; (1761)..(2273)

&lt;223&gt; calcineurin B

&lt;400&gt; 23

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Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly
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 <211> 535  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
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 35 40 45  
 Leu Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp  
 50 55 60  
 Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile  
 65 70 75 80  
 Ala Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys  
 85 90 95  
 Thr Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His  
 100 105 110  
 Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro  
 115 120 125  
 Ala Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr  
 130 135 140  
 Phe Ser Ile Glu Cys Val Leu Tyr Leu Trp Val Leu Lys Ile Leu Tyr  
 145 150 155 160  
 Pro Ser Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg His Leu  
 165 170 175  
 Thr Glu Tyr Phe Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser Glu  
 180 185 190  
 Arg Val Tyr Glu Ala Cys Met Glu Ala Phe Asp Ser Leu Pro Leu Ala  
 195 200 205  
 Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly Leu Ser Pro  
 210 215 220  
 Glu Ile His Thr Leu Asp Asp Ile Arg Arg Leu Asp Arg Phe Lys Glu

225                      230                      235                      240  
 Pro Pro Ala Phe Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Ser  
                                  245                      250                      255  
 Glu Asp Phe Gly Asn Glu Lys Ser Gln Glu His Phe Ser His Asn Thr  
                                  260                      265                      270  
 Val Arg Gly Cys Ser Tyr Phe Tyr Asn Tyr Pro Ala Val Cys Glu Phe  
                                  275                      280                      285  
 Leu Gln Asn Asn Asn Leu Leu Ser Ile Ile Arg Ala His Glu Ala Gln  
                                  290                      295                      300  
 Asp Ala Gly Tyr Arg Met Tyr Arg Lys Ser Gln Thr Thr Gly Phe Pro  
 305                      310                      315                      320  
 Ser Leu Ile Thr Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val Tyr Asn  
                                  325                      330                      335  
 Asn Lys Ala Ala Val Leu Lys Tyr Glu Asn Asn Val Met Asn Ile Arg  
                                  340                      345                      350  
 Gln Phe Asn Cys Ser Pro His Pro Tyr Trp Leu Pro Asn Phe Met Asp  
                                  355                      360                      365  
 Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val Thr Glu Met  
                                  370                      375                      380  
 Leu Val Asn Val Leu Ser Ile Cys Ser Asp Asp Glu Leu Met Thr Glu  
 385                      390                      395                      400  
 Gly Glu Asp Gln Phe Asp Gly Ser Ala Ala Ala Arg Lys Glu Ile Ile  
                                  405                      410                      415  
 Arg Asn Lys Ile Arg Ala Ile Gly Lys Met Ala Arg Val Phe Ser Val  
                                  420                      425                      430  
 Leu Arg Glu Glu Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr Pro  
                                  435                      440                      445  
 Thr Gly Met Leu Pro Ser Gly Val Leu Ala Gly Gly Arg Gln Thr Leu  
                                  450                      455                      460  
 Gln Ser Ala Thr Val Glu Ala Ile Glu Ala Glu Lys Ala Ile Arg Gly  
 465                      470                      475                      480  
 Phe Ser Pro Pro His Arg Ile Cys Ser Phe Glu Glu Ala Lys Gly Leu  
                                  485                      490                      495  
 Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Lys Asp Ala Val Gln Gln  
                                  500                      505                      510  
 Asp Gly Phe Asn Ser Leu Asn Thr Ala His Ala Thr Glu Asn His Gly  
                                  515                      520                      525  
 Thr Gly Asn His Thr Ala Gln  
                                  530                      535

&lt;210&gt; 25

&lt;211&gt; 170

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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Xaa Asp Glu Ile Lys Arg Leu Gly Lys Arg Phe Lys Lys Xaa Asp Leu  
 20 25 30

Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Xaa Pro Glu  
 35 40 45

Leu Gln Gln Asn Xaa Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
 50 55 60

Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Xaa Val Ser  
 65 70 75 80

Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
 85 90 95

Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
 100 105 110

Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
 115 120 125

Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Xaa  
 130 135 140

Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Xaa Gly Leu  
 145 150 155 160

Asp Ile His Lys Lys Met Val Val Asp Val  
 165 170

&lt;210&gt; 26

&lt;211&gt; 5611

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (115)..(1776)

&lt;223&gt; histidine tagged calcineurin A beta2

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1777)..(1814)

&lt;223&gt; ribosomal binding site, multiple cloning site 2

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1815)..(2327)

&lt;223&gt; calcineurin B

&lt;400&gt; 26

ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60

attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aact atg 117  
Met  
1

aga gga tcg cat cac cat cac cat cac gga tcc gcc gcc ccg gag ccg 165  
Arg Gly Ser His His His His His His Gly Ser Ala Ala Pro Glu Pro  
5 10 15

gcc cgg gct gca ccg ccc cca ccc ccg ccc ccg ccg ccc cct ccc ggg 213  
Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly  
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gct gac cgc gtc gtc aaa gct gtc cct ttc ccc cca aca cat cgc ttg 261  
Ala Asp Arg Val Val Lys Ala Val Pro Phe Pro Pro Thr His Arg Leu  
35 40 45

aca tct gaa gaa gta ttt gat ttg gat ggg ata ccc agg gtt gat gtt 309  
Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp Val  
50 55 60 65

ctg aag aac cac ttg gtg aaa gaa ggt cga gta gat gaa gaa att gcg 357  
Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile Ala  
70 75 80

ctt aga att atc aat gag ggt gct gcc atc ctt cgg aga gag aaa acc 405  
Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys Thr  
85 90 95

atg ata gaa gta gaa gct cca atc aca gtg tgt ggt gac atc cat ggc 453  
Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His Gly  
100 105 110

caa ttt ttt gat ctg atg aaa ctt ttt gaa gta gga gga tca cct gct 501  
Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro Ala  
115 120 125

aat aca cga tac ctt ttt ctt ggc gat tat gtg gac aga ggt tat ttt 549  
Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr Phe  
130 135 140 145

agt ata gag cat gtt cta ggc act gaa gac ata tcg att aat cct cac 597  
Ser Ile Glu His Val Leu Gly Thr Glu Asp Ile Ser Ile Asn Pro His  
150 155 160

aat aat att aat gag tgt gtc tta tat tta tgg gtt ctg aag att cta 645  
Asn Asn Ile Asn Glu Cys Val Leu Tyr Leu Trp Val Leu Lys Ile Leu  
165 170 175

tac cca agc aca tta ttt ctt ctg aga ggc aac cat gaa tgc aga cac 693  
Tyr Pro Ser Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys Arg His  
180 185 190

ctt act gaa tat ttt acc ttt aag cag gaa tgt aaa att aag tat tcg 741  
Leu Thr Glu Tyr Phe Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr Ser  
195 200 205

gaa aga gtc tat gaa gct tgt atg gaa gct ttt gat agt ttg cct ctt 789  
Glu Arg Val Tyr Glu Ala Cys Met Glu Ala Phe Asp Ser Leu Pro Leu  
210 215 220 225

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tct gaa gat ttt gga aat gaa aaa tca cag gaa cat ttt agt cac aat Ser Glu Asp Phe Gly Asn Glu Lys Ser Gln Glu His Phe Ser His Asn 275 280 285			981
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cct tca tta ata aca att ttt tcg gca cct aat tac tta gat gtc tac Pro Ser Leu Ile Thr Ile Phe Ser Ala Pro Asn Tyr Leu Asp Val Tyr 340 345 350			1173
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 Gly Phe Ser Pro Pro His Arg Ile Cys Ser Phe Glu Glu Ala Lys Gly  
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ttg gat agg atc aat gag aga atg cca cct cgg aaa gat gct gta cag 1701  
 Leu Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Lys Asp Ala Val Gln  
 515 520 525

caa gat ggt ttc aat tct ctg aac acc gca cat gcc act gag aac cac 1749  
 Gln Asp Gly Phe Asn Ser Leu Asn Thr Ala His Ala Thr Glu Asn His  
 530 535 540 545

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 Gly Thr Gly Asn His Thr Ala Gln  
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 Met Gly Asn Glu Ala Ser Tyr Pro Leu Glu Met  
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 Cys Ser His Phe Asp Xaa Asp Glu Ile Lys Arg Leu Gly Lys Arg Phe  
 570 575 580

aag aag cty gat ttg gac aat tct ggt tct ttg agt gtg gaa gag ttc 1943  
 Lys Lys Xaa Asp Leu Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe  
 585 590 595

atg tct ctr cct gag tta caa cag aat ccy tta gta cag cga gta ata 1991  
 Met Ser Xaa Pro Glu Leu Gln Asn Xaa Leu Val Gln Arg Val Ile  
 600 605 610

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 Asp Ile Phe Asp Thr Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe  
 615 620 625

att gag ggm gtc tct cag ttc agt gtc aaa gga gat aag gar cag aar 2087  
 Ile Glu Xaa Val Ser Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys  
 630 635 640 645

ttg agg ttt gct ttc cgt atc tat gac atg gat aaa gay ggc tat att 2135  
 Leu Arg Phe Ala Phe Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile  
 650 655 660

tcc aat ggg gaa ctc ttc cag gtr ytr aag atg atg gtg ggg aac aat 2183  
 Ser Asn Gly Glu Leu Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn  
 665 670 675

ctg aaa gat aca cag tta cag caa att gta gac aaa acc ata ata aat 2231  
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 680 685 690

gca gat aag gat ggr gat gga aga ata tcc ttt gaa gaa ttc tgt gct 2279  
 Ala Asp Lys Asp Xaa Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala  
 695 700 705

gtt gta ggy ggc cta gat atc cac aaa aag atg gtg gta gat gtg tga 2327  
 Val Val Xaa Gly Leu Asp Ile His Lys Lys Met Val Val Asp Val

710 715 720 725

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&lt;210&gt; 27

&lt;211&gt; 553

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 27

Met Arg Gly Ser His His His His His Gly Ser Ala Ala Pro Glu  
 1 5 10 15

Pro Ala Arg Ala Ala Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro  
 20 25 30

Gly Ala Asp Arg Val Val Lys Ala Val Pro Phe Pro Pro Thr His Arg  
 35 40 45  
 Leu Thr Ser Glu Glu Val Phe Asp Leu Asp Gly Ile Pro Arg Val Asp  
 50 55 60  
 Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Val Asp Glu Glu Ile  
 65 70 75 80  
 Ala Leu Arg Ile Ile Asn Glu Gly Ala Ala Ile Leu Arg Arg Glu Lys  
 85 90 95  
 Thr Met Ile Glu Val Glu Ala Pro Ile Thr Val Cys Gly Asp Ile His  
 100 105 110  
 Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val Gly Gly Ser Pro  
 115 120 125  
 Ala Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp Arg Gly Tyr  
 130 135 140  
 Phe Ser Ile Glu His Val Leu Gly Thr Glu Asp Ile Ser Ile Asn Pro  
 145 150 155 160  
 His Asn Asn Ile Asn Glu Cys Val Leu Tyr Leu Trp Val Leu Lys Ile  
 165 170 175  
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 His Leu Thr Glu Tyr Phe Thr Phe Lys Gln Glu Cys Lys Ile Lys Tyr  
 195 200 205  
 Ser Glu Arg Val Tyr Glu Ala Cys Met Glu Ala Phe Asp Ser Leu Pro  
 210 215 220  
 Leu Ala Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly Leu  
 225 230 235 240  
 Ser Pro Glu Ile His Thr Leu Asp Asp Ile Arg Arg Leu Asp Arg Phe  
 245 250 255  
 Lys Glu Pro Pro Ala Phe Gly Pro Met Cys Asp Leu Leu Trp Ser Asp  
 260 265 270  
 Pro Ser Glu Asp Phe Gly Asn Glu Lys Ser Gln Glu His Phe Ser His  
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 Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr Asn Tyr Pro Ala Val Cys  
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- 67 -

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 385                      390                      395                      400  
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 Thr Glu Gly Glu Asp Gln Phe Asp Gly Ser Ala Ala Ala Arg Lys Glu  
 420                      425                      430  
 Ile Ile Arg Asn Lys Ile Arg Ala Ile Gly Lys Met Ala Arg Val Phe  
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 Ser Val Leu Arg Glu Glu Ser Glu Ser Val Leu Thr Leu Lys Gly Leu  
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 Thr Pro Thr Gly Met Leu Pro Ser Gly Val Leu Ala Gly Gly Arg Gln  
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 485                      490                      495  
 Arg Gly Phe Ser Pro Pro His Arg Ile Cys Ser Phe Glu Glu Ala Lys  
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 Gly Leu Asp Arg Ile Asn Glu Arg Met Pro Pro Arg Lys Asp Ala Val  
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 20                      25                      30  
 Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Xaa Pro Glu  
 35                      40                      45  
 Leu Gln Gln Asn Xaa Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
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 Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Xaa Val Ser  
 65                      70                      75                      80  
 Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
 85                      90                      95

Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
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Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
 115 120 125

Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Xaa  
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Asp Ile His Lys Lys Met Val Val Asp Val  
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 Met  
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aga gga tcg cat cac cat cac cat cac gga tcc atg tcc ggg agg cgc 165  
 Arg Gly Ser His His His His His Gly Ser Met Ser Gly Arg Arg  
 5 10 15

ttc cac ctc tcc acc acc gac cgc gtc atc aaa gct gtc ccc ttt cct 213  
 Phe His Leu Ser Thr Thr Asp Arg Val Ile Lys Ala Val Pro Phe Pro  
 20 25 30

cca acc caa cgg ctt act ttc aag gaa gta ttt gag aat ggg aaa cct 261  
 Pro Thr Gln Arg Leu Thr Phe Lys Glu Val Phe Glu Asn Gly Lys Pro  
 35 40 45

aaa gtt gat gtt tta aaa aac cat ttg gta aag gaa gga cga ctg gaa 309  
 Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu Glu  
 50 55 60 65

gag gaa gta gcc tta aag ata atc aat gat ggg gct gcc atc ctg agg 357

**SUBSTITUTE SHEET (RULE 26)**

gtc tat aac aat aaa gct gct gtg ttg aaa tat gaa aac aat gtc atg 1125  
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aat atc agg cag ttt aac tgt tct cca cac ccc tac tgg ctt cca aac 1173  
 Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro Tyr Trp Leu Pro Asn  
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 Arg Lys Asp Ser Ile Tyr Pro Gly Gly Pro Met Lys Ser Val Thr Ser  
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gca cac tca cat gct gcg cac agg agc gac caa ggg aag aaa gcc cat 1653  
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 Pro Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu  
 50 55 60  
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 65 70 75 80  
 Arg Gln Glu Lys Thr Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys  
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 Gly Asp Ile His Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val  
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 Lys Ile Asn His Pro Lys Thr Leu Phe Leu Leu Arg Gly Asn His Glu  
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 Cys Arg His Leu Thr Asp Tyr Phe Thr Phe Lys Gln Glu Cys Arg Ile  
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 Lys Tyr Ser Glu Gln Val Tyr Asp Ala Cys Met Glu Thr Phe Asp Cys

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 Gly Met Ser Pro Glu Ile Thr Ser Leu Asp Asp Ile Arg Lys Leu Asp  
 210 215 220  
 Arg Phe Thr Glu Pro Pro Ala Phe Gly Pro Val Cys Asp Leu Leu Trp  
 225 230 235 240  
 Ser Asp Pro Ser Glu Asp Tyr Gly Asn Glu Lys Thr Leu Glu His Tyr  
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 260 265 270  
 Val Cys Glu Phe Leu Gln Asn Asn Asn Leu Leu Ser Ile Ile Arg Ala  
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 Val Thr Glu Met Leu Val Asn Val Leu Asn Ile Cys Ser Asp Asp Glu  
 370 375 380  
 Leu Ile Ser Asp Asp Glu Ala Glu Gly Ser Thr Thr Val Arg Lys Glu  
 385 390 395 400  
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 Thr Ile Glu Thr Ala Ile Arg Gly Phe Ser Leu Gln His Lys Ile Arg  
 450 455 460  
 Ser Phe Glu Glu Ala Arg Gly Leu Asp Arg Ile Asn Glu Arg Met Pro  
 465 470 475 480  
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His Ser

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 35 40 45  
 Leu Gln Gln Asn Pro Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
 50 55 60  
 Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Gly Val Ser  
 65 70 75 80  
 Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
 85 90 95  
 Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
 100 105 110  
 Phe Gln Val Leu Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
 115 120 125  
 Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Gly  
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&lt;223&gt; ribosomal binding site, multiple cloning site 2

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&lt;222&gt; (1732)..(2244)

&lt;223&gt; calcineurin B

&lt;220&gt;

&lt;221&gt; variation

&lt;222&gt; (1474)..(1503)

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 cytoskeleton, death-domain homolog, stomatin  
 homolog

&lt;400&gt; 32

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                                     Met
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Phe His Leu Ser Thr Thr Asp Arg Val Ile Lys Ala Val Pro Phe Pro
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cca acc caa cgg ctt act ttc aag gaa gta ttt gag aat ggg aaa cct      261
Pro Thr Gln Arg Leu Thr Phe Lys Glu Val Phe Glu Asn Gly Lys Pro
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Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu Glu
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Glu Glu Val Ala Leu Lys Ile Ile Asn Asp Gly Ala Ala Ile Leu Arg
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caa gag aag act atg ata gaa gta gat gct cca atc aca gta tgt ggt      405
Gln Glu Lys Thr Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys Gly
                85                      90                      95

gat att cat gga caa ttc ttt gac cta atg aag tta ttt gaa gtt gga      453
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Gly Ser Pro Ser Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val Asp
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Arg Gly Tyr Phe Ser Ile Glu Cys Val Leu Tyr Leu Trp Ser Leu Lys
                130                      135                      140                      145

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Ile Asn His Pro Lys Thr Leu Phe Leu Leu Arg Gly Asn His Glu Cys
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agg cat ctt aca gac tat ttc acc ttc aaa cag gaa tgt cga atc aaa      645
Arg His Leu Thr Asp Tyr Phe Thr Phe Lys Gln Glu Cys Arg Ile Lys
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tat tcg gaa cag gtg tat gat gcc tgt atg gag aca ttt gac tgt ctt      693

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Pro Leu Ala Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly Gly	
195 200 205	
atg tca cct gaa att act tct tta gat gac att agg aaa tta gac agg	789
Met Ser Pro Glu Ile Thr Ser Leu Asp Asp Ile Arg Lys Leu Asp Arg	
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Phe Thr Glu Pro Pro Ala Phe Gly Pro Val Cys Asp Leu Leu Trp Ser	
230 235 240	
gat ccc tca gag gat tat ggc aat gag aag acc ttg gag cac tat acc	885
Asp Pro Ser Glu Asp Tyr Gly Asn Glu Lys Thr Leu Glu His Tyr Thr	
245 250 255	
cac aac act gtc cga ggg tgc tct tat ttc tac agt tac cct gca gtt	933
His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr Ser Tyr Pro Ala Val	
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Cys Glu Phe Leu Gln Asn Asn Asn Leu Leu Ser Ile Ile Arg Ala His	
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gaa gcc caa gat gct ggg tat cga atg tac agg aag agc caa gcc aca	1029
Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr Arg Lys Ser Gln Ala Thr	
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Val Tyr Asn Asn Lys Ala Ala Val Leu Lys Tyr Glu Asn Asn Val Met	
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Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro Tyr Trp Leu Pro Asn	
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Phe Met Asp Val Phe Thr Trp Ser Leu Pro Phe Val Gly Glu Lys Val	
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Thr Glu Met Leu Val Asn Val Leu Asn Ile Cys Ser Asp Asp Glu Leu	
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att tct gat gat gaa gca gaa gga agc act aca gtt cgt aag gag atc	1317
Ile Ser Asp Asp Glu Ala Glu Gly Ser Thr Thr Val Arg Lys Glu Ile	
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Ile Leu Arg Gln Glu Ser Glu Ser Val Leu Thr Leu Lys Gly Leu Thr	
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 His Arg Ser Asp Gln Gly Lys Lys Ala His Ser  
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&lt;211&gt; 524



&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 33

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Pro Lys Val Asp Val Leu Lys Asn His Leu Val Lys Glu Gly Arg Leu
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Glu Glu Glu Val Ala Leu Lys Ile Ile Asn Asp Gly Ala Ala Ile Leu
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Arg Gln Glu Lys Thr Met Ile Glu Val Asp Ala Pro Ile Thr Val Cys
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Gly Asp Ile His Gly Gln Phe Phe Asp Leu Met Lys Leu Phe Glu Val
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Gly Gly Ser Pro Ser Asn Thr Arg Tyr Leu Phe Leu Gly Asp Tyr Val
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Asp Arg Gly Tyr Phe Ser Ile Glu Cys Val Leu Tyr Leu Trp Ser Leu
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Lys Ile Asn His Pro Lys Thr Leu Phe Leu Leu Arg Gly Asn His Glu
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Cys Arg His Leu Thr Asp Tyr Phe Thr Phe Lys Gln Glu Cys Arg Ile
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Lys Tyr Ser Glu Gln Val Tyr Asp Ala Cys Met Glu Thr Phe Asp Cys
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Leu Pro Leu Ala Ala Leu Leu Asn Gln Gln Phe Leu Cys Val His Gly
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Ser Asp Pro Ser Glu Asp Tyr Gly Asn Glu Lys Thr Leu Glu His Tyr
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Thr His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr Ser Tyr Pro Ala
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Val Cys Glu Phe Leu Gln Asn Asn Asn Leu Leu Ser Ile Ile Arg Ala
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Thr Gly Phe Pro Ser Leu Ile Thr Ile Phe Ser Ala Pro Asn Tyr Leu

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<212> PRT
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Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Leu Pro Glu
          35           40           45
Leu Gln Gln Asn Pro Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr
          50           55           60
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 65           70           75           80

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Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
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Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
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Phe Gln Val Leu Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
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Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Gly  
                                     130                                    135                                    140

Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Gly Gly Leu  
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<222> (15)

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